

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 04:18:20 ; Search time 1817.87 Seconds
(without alignments)
12340.402 Million cell updates/sec

Title: US-09-811-118-2

Perfect score: 1072
Sequence: 1 GAGCGCGCCACCTCCGGAAC.....TTGCATCAACATGATTTTC 1072

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_Da:*
2: gb_Htg:*
3: gb_In:*
4: gb_Om:*
5: gb_Ov:*
6: gb_Pat:*
7: gb_Pn:*
8: gb_Pl:*
9: gb_Pr:*
10: gb_Ro:*
11: gb_Sts:*
12: gb_Sy:*
13: gb_Un:*
14: gb_Vl:*
15: em_Ba:*
16: em_Fun:*
17: em_Hum:*
18: em_In:*
19: em_Mu:*
20: em_Om:*
21: em_Or:*
22: em_Ov:*
23: em_Pat:*
24: em_Ph:*
25: em_Pl:*
26: em_Ro:*
27: em_Sts:*
28: em_Un:*
29: em_Vl:*
30: em_Htg_Hum:*
31: em_Htg_Inv:*
32: em_Htg_Other:*
33: em_Htgo_Inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
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1	1072	100.0	1072	6	AR151077	AR151077 Sequence
2	1067.2	99.6	1228	9	AK027683	AK027683 Homo sapi
3	1067.2	99.6	1511	6	AX188360	AX188360 Sequence
4	1064.2	99.3	1227	6	AX080813	AX080813 Sequence
5	1035.4	96.6	1251	6	AX080809	AX080809 Sequence
6	809.2	75.5	857	9	AF091092	AF091092 Homo sapi
7	645.4	60.2	160066	2	AL356976	AL356976 Homo sapi
8	473	44.1	1033	10	BC003228	BC003228 Mus muscu
9	435.4	40.6	51381	2	AF322456	AF322456 Homo sapi
10	406.2	37.9	751	6	AX186595	AX186595 Sequence
11	356	33.2	468	6	AX187668	AX187668 Sequence
12	261.8	24.4	51381	2	AF322456	AF322456 Homo sapi
13	217	20.2	241048	2	AL627238	AL627238 Mus muscu
14	177.2	16.5	1047	10	BC019664	BC019664 Mus muscu
15	174.6	16.3	55891	2	AC022847	AC022847 Homo sapi
16	125	11.7	164683	2	AC097883	AC097883 Rattus no
17	115.4	10.8	164683	2	AC097883	AC097883 Rattus no
18	106.2	9.9	9970	1	AE004709	AE004709 Pseudomon
19	106	9.9	203050	1	AE005847	AE005847 Caulobact
20	105.4	9.8	10886	1	AE005847	AE005847 Caulobact
21	104.8	9.8	151813	2	AC026737	AC026737 Homo sapi
22	104.8	9.8	171307	2	AL355820	AL355820 Homo sapi
23	104.8	9.8	176507	2	AC025790	AC025790 Homo sapi
24	104.8	9.8	183494	9	AC091977	AC091977 Homo sapi
25	99.4	9.3	915	8	HV0238745	HV0238745 Homo sapi
26	98	9.1	13404	2	AF322452	AF322452 Homo sapi
27	97.2	8.7	13404	2	AF322452	AF322452 Homo sapi
28	93.6	8.5	701	3	SCMG1978	SCMG1978 Homo sapi
29	91.6	8.5	984	8	AB009083	AB009083 Chlamydom
30	91.4	8.5	890	8	AF242650	AF242650 Hevea bra
31	90.2	8.4	40969	1	SCD6	SCD6 Streptomy
32	90	8.4	196050	1	AL646058	AL646058 Ralstonia
33	89.6	8.4	1026	8	HV0238697	HV0238697 Homo sapi
34	89.2	8.3	363	11	G71688	G71688 Arabidops
35	89.2	8.3	921	8	OSR270955	OSR270955 Oryza sat
36	86.4	8.1	265383	2	AC020874	AC020874 Mus muscu
37	86.4	7.9	3169	1	EC000266	EC000266 Escherich
38	84.4	7.9	10558	1	AE005394	AE005394 Escherich
39	84.4	7.9	10561	1	D90814	D90814 E. coli geno
40	84.4	7.9	19031	1	D90814	D90814 E. coli geno
41	84.4	7.9	19273	1	D90813	D90813 E. coli geno
42	84.4	7.9	257071	1	AP002558	AP002558 Pseudomon
43	84.2	7.9	10647	1	AE004518	AE004518 Pseudomon
44	83.4	7.8	871	8	AF322903	AF322903 Rhipanus
45	83.4	7.8	871	8	AF322903	AF322903 Rhipanus

ALIGNMENTS

RESULT 1	AR151077	Sequence 2 from patent US 6231853.	1072 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	AR151077	Sequence 2 from patent US 6231853.	1072 bp	DNA	linear	PAT 08-AUG-2001
DEFINITION	AR151077	Sequence 2 from patent US 6231853.	1072 bp	DNA	linear	PAT 08-AUG-2001
ACCESSION	AR151077	Sequence 2 from patent US 6231853.	1072 bp	DNA	linear	PAT 08-AUG-2001
VERSION	AR151077.1	GI:15117127	1072 bp	DNA	linear	PAT 08-AUG-2001
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1072)					
AUTHORS	Hillman,J.L., Corley,N.C. and Patterson,C.					
TITLE	Human glutathione peroxidase-6					
JOURNAL	Patent: US 6231853-A 2 15-MAY-2001.					
FEATURES	Location/Qualifiers					
SOURCE	1..1072					
BASE COUNT	275 a 294 c 270 g 233 t					
ORIGIN	/Organism="unknown"					
Query Match	100.0%	Score 1072;	DB 6;	Length 1072;		
Best Local Similarity	100.0%;	Pred. No. 3,2e-231;				

Db 1056 GAACCTCTGGCCCAATGAGAGCTCTTGACCAGTGAATCACAGCCGCAATAGCAAGCTCTG 1115
QY 841 CAACAAAATGTGTGGCAATATAGATATATCAAGCAATATATCTCCACCAAGGCTCT 900
Db 1116 CAACAAAATGTGTGGCAATATAGATATATCAAGCAATATATCTCCACCAAGGCTCT 1175
QY 901 GTAACTGGGACCAATGATTAATCTATAGAGCTGTGTGAGATTTAGATGAATACCTG 960
Db 1176 GTAACTGGGACCAATGATTAATCTATAGAGCTGTGTGAGATTTAGATGAATACCTG 1235
QY 961 TGAAGTGCCTAGCAGTGCAGCCCAATATAGAGGATTCATATGAACATTTTTCATAT 1020
Db 1236 TGAAGTGCCTAGCAGTGCAGCCCAATATAGAGGATTCATATGAACATTTTTCATAT 1295
QY 1021 AAACCAAAAATATCTGTATATCAATTAACATTCATCCACATGATTTTC 1072
Db 1296 AAACCAAAAATATCTGTATATCAATTAACATTCATCCACATGATTTTC 1347

RESULT 4
AX080813 1227 bp DNA linear PAT 27-FEB-2001
LOCUS Sequence 59 from Patent WO0109327.
AX080813
VERSION AX080813.1 GI:13169783
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1227)
AUTHORS Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L.,
Kljava,I.J., Lafleur,M., Mark,M.R., Marsters,S.A., Plitt,R.M.,
Matanabe,C.K. and Wood,W.I.
Method of preventing the injury or death of retinal cells and
treating ocular diseases
Patent: WO 0109327-A 59 08-FEB-2001;
JOURNAL Genentech, Inc. (US)
FEATURES
source 1.1227
Location/Qualifiers
BASE COUNT 331 a 325 c 293 g 278 t
ORIGIN

Query Match 99.3%; Score 1064.2; DB 6; Length 1227;
Best Local Similarity 99.7%; Pred. No. 1.8e-229;
Matches 1066; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 364 CATGTTAGCAGATGTCAGTACCGGTACTGTGCGCATTCCTGCTTCAATACCTGAGC 423
Db 372 CATGTTAGCAGATGTCAGTACCGGTACTGTGCGCATTCCTGCTTCAATACCTGAGC 431
QY 424 CCAGACTTGTGGAGAGAGCCCACTGTGAACCTTGTGAAGTACTAGTAGACCCAGATG 483
Db 432 CCAGACTTGTGGAGAGAGCCCACTGTGAACCTTGTGAAGTACTAGTAGACCCAGATG 491
QY 484 AAGGTGTAGAGGCTTGTGGACCACTGTGAGTGGAGGAGGTGACAGTCCAGATCAG 543
Db 492 AAGGTGTAGAGGCTTGTGGACCACTGTGAGTGGAGGAGGTGACAGTCCAGATCAG 551
QY 544 AGGCTGTGAGAGAGCTATCTACTGAAGGAGAGAGCTTATACCAACCGGCTCTCT 603
Db 552 AGGCTGTGAGAGAGCTATCTACTGAAGGAGAGAGCTTATACCAACCGGCTCTCT 611
QY 604 CCTCCACACCTTCATCCCGCCCACTGTGTGGGCTGACCAATGCAAACTCAATGTGC 663
Db 612 CCTCCACACCTTCATCCCGCCCACTGTGTGGGCTGACCAATGCAAACTCAATGTGC 671
QY 664 TTCAAGGGAGAGAGCCAGTCTCTCTTCTTCTATGACATTTGCTCCATCAT 723
Db 672 TTCAAGGGAGAGAGCCAGTCTCTCTTCTTCTATGACATTTGCTCCATCAT 731
QY 724 TCTTGTGGGGGAAAAATTTAGTATTTTGAATTTTGAATCTTACAGCAAAATAGAA 783
Db 732 TCTTGTGGGGGAAAAATTTAGTATTTTGAATTTTGAATCTTACAGCAAAATAGAA 791
QY 784 CTCTGTGGCAATAGAGCTTGTACAGTGAATCAGAGCGGCTAGGAAGCTTGTGCA 843
Db 792 CTCTGTGGCAATAGAGCTTGTACAGTGAATCAGAGCGGCTAGGAAGCTTGTGCA 851
QY 844 CAAAATATGTGGCAATATAGATATATCAAGCAATATCTCCACCAAGGCTTGTGA 903
Db 852 CAAAATATGTGGCAATATAGATATATCAAGCAATATCTCCACCAAGGCTTGTGA 911
QY 904 AACTGGAGCAATGATTACTCTATAGGCTGTGTGAGATTTAGATGAATACCTGTGA 963
Db 912 AACTGGAGCAATGATTACTCTATAGGCTGTGTGAGATTTAGATGAATACCTGTGA 971
QY 964 AAGTGCCTAGCAGTGCAGCCCAATATAGAGGATTCATTAAGCAATTTTTCATATA 1023
Db 972 AAGTGCCTAGCAGTGCAGCCCAATATAGAGGATTCATTAAGCAATTTTTCATATA 1031
QY 1024 CCAAAAATATCTTGTATCAATTAACATTTGATCCACATGAATTTTC 1072
Db 1032 CCAAAAATATCTTGTATCAATTAACATTTGATCCACATGAATTTTC 1080

RESULT 5
AX080809 1251 bp DNA linear PAT 27-FEB-2001
LOCUS Sequence 55 from Patent WO0109327.
AX080809
DEFINITION AX080809
ACCESSION AX080809
VERSION AX080809.1 GI:13169779
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 1251)
AUTHORS Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L.,
Kljava,I.J., Lafleur,M., Mark,M.R., Marsters,S.A., Plitt,R.M.,
Matanabe,C.K. and Wood,W.I.
Method of preventing the injury or death of retinal cells and
treating ocular diseases
Patent: WO 0109327-A 55 08-FEB-2001;
JOURNAL Genentech, Inc. (US)
FEATURES
source 1.1251
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Partial DNA sequence used to isolate DNA57037."

unsure 1231

/note="unknown base"

BASE COUNT 343 a 328 c 298 g 280 t 2 others

ORIGIN

Query Match

96.6%; Score 1035.4; DB 6; Length 1251;

Best Local Similarity 99.4%; Pred. No. 5.7e-223;

Matches 1069; Conservative 1; Mismatches 2; Indels 3; Gaps 3;

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QY 1 GAGCGCGCCACCTCCGGCAACAGCCATGTTGGGGGCGGAGCGTGGGCGGCGGCTGCT 60
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Db 4 GAGCGCGCCACCTCCGGCAACAGCCATGTTGGGGGCGGAGCGTGGGCGGCGGCTGCT 63
QY 61 CCTGTGGCTGGGGCTGGCGGCGAGAGAGAGAGACTTCTAGACTTCAAGCGGCTCA 120
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Db 64 CCTGTGGCTGGGGCTGGCGGCGAGAGAGAGAGACTTCTAGACTTCAAGCGGCTCA 123
QY 121 CATCCGGGGCAAACTGTGTGCTGAGAAATACCGCGGATCGGTGCTCCCTGGTGTGAA 180
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Db 124 CATCCGGGGCAAACTGTGTGCTGAGAAATACCGCGGATCGGTGCTCCCTGGTGTGAA 183
QY 181 TGTGGCCACGAGTGGGGCTTCACACACGAGCTACCGAGCCCTGAGAGCTGACGCG 240
   |||||||
Db 184 TGTGGCCACGAGTGGGGCTTCACACACGAGCTACCGAGCCCTGAGAGCTGACGCG 243
QY 241 AGACCTGGGGCCCCCACCCTTCAAGCTGCTGCGCTCCCTGCAACGAGTTTGGCCACA 300
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Db 244 AGACCTGGGGCCCCCACCCTTCAAGCTGCTGCGCTCCCTGCAACGAGTTTGGCCACA 303
QY 301 GGAAGCTGACAGCAACAGAGAGATTGAGAGCTTTGCCCTGCCGACCTACAGTGTG-TCAT 359
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Db 304 GGAAGCTGACAGCAACAGAGAGATTGAGAGCTTTGCCCTGCCGACCTACAGTGTGTCAT 363
QY 360 TCCCCATGTTTA-GCAAGATTGACGTCACCGGACT-GGTGGCCATCTCCCTTCAAGTA 417
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Db 364 TCCCCATGTTTAAAGATTGACGTCACCGGACTGAGTGGGGCCATCTCCCTTCAAGTA 423
QY 418 CCTGGCCACGACTTCTGGGAGAGAGCCACCTGGAATCTTGGAGATACCTAGTAGCCCC 477
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Db 424 CCTGGCCACGACTTCTGGGAGAGAGCCACCTGGAATCTTGGAGATACCTAGTAGCCCC 483
QY 478 AGATGAAAGGTGTAGGGGCTTGGAGCCCACTGTGTCAAGTGGAGAGGTGACACTCA 537
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Db 484 AGATGAAAGGTGTAGGGGCTTGGAGCCCACTGTGTCAAGTGGAGAGGTGACACTCA 543
QY 538 GATCAAGAGGCTGTGAGAGAGAGTCACTCACTGAAGCGGAGAGACTTATAACCCGCG 597
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Db 544 GATCAAGAGGCTGTGAGAGAGAGTCACTCACTGAAGCGGAGAGACTTATAACCCGCG 603
QY 598 TCTCTCTCTCACACACCTATCCGCGCCACTGTGTGGGGCTGACCAATGCAAACTCAA 657
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Db 604 TCTCTCTCTCACACACCTATCCGCGCCACTGTGTGGGGCTGACCAATGCAAACTCAA 663
QY 658 TGTGCTTCAAGGAGAGAGACCACTGACTCTCTCTCTTACTCTTATGCAATTGGTCC 717
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Db 664 TGTGCTTCAAGGAGAGAGACCACTGACTCTCTCTCTTACTCTTATGCAATTGGTCC 723
QY 718 CATCATCTCTTGGGGGAAAAATTTAGTATTTTGAATTTATTTAACTTACACACAAA 777
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Db 724 CATCATCTCTTGGGGGAAAAATTTAGTATTTTGAATTTATTTAACTTACACACAAA 783
QY 778 TAGGAAGTCTGTGGCCATGAGAGCTTGTGACCAATACAGCGATACGAGCTCT 837
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Db 784 TAGGAAGTCTGTGGCCATGAGAGCTTGTGACCAATACAGCGATACGAGCTCT 843
QY 838 TGGCAACAAAAATGTGTGCAATAGAGATATCAAGCAATATCTCCACCCAAAGCT 897
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Db 844 TGGCAACAAAAATGTGTGCAATAGAGATATCAAGCAATATCTCCACCCAAAGCT 903
QY 898 TCTGTAAAGTGGGAGCAATGATTACCTAATAGGGGCTGTGTGAGAGTTAGAGAAATAC 957
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Db 904 TCTGTAAAGTGGGAGCAATGATTACCTAATAGGGGCTGTGTGAGAGTTAGAGAAATAC 963

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QY 958 CTGTGAAAGTGCCTAGGACATGCGCAGCCAAATAGAGGCAATGAAACATTTTGGCA 1017
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QY 1018 TATTAACCAAAAAATATCTGTTATCATATAAAACTTGCATCCACATGATTTTC 1072
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Db 1024 TATTAACCAAAAAATATCTGTTATCATATAAAACTTGCATCCACATGATTTTC 1078

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RESULT 6

AF091092 857 bp mRNA linear PRI 12-NOV-1998
 LOCUS Homo sapiens clone 683 unknown mRNA, complete sequence.
 DEFINITION AF091092
 ACCESSION AF091092.1 GI:3860021
 VERSION FLI_CDNA.
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 857)
 Barrow, I.K., -P., Boguski, M.S., Touchman, J. and Spencer, F.
 TITLE Full-insert sequence of mapped XREF EST
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 857)
 Barrow, I.K., -P., Boguski, M.S., Touchman, J. and Spencer, F.
 TITLE Direct Submission
 JOURNAL Submitted (31-AUG-1998) NHGRI, NIH, 49 Convent Drive, Building 49,
 Room 2C08, Bethesda, MD 20892, USA

FEATURES
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 /chromosome="1"
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 /clone="683"
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 with mouse locus D1Xrf379"
 46..225
 /note="similar to Saccharomyces cerevisiae ORF YBR24W"
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CDS

BASE COUNT 267 a 216 c 184 g 190 t
 ORIGIN

Query Match 75.5%; Score 809.2; DB 9; Length 857;
 Best Local Similarity 99.6%; Pred. No. 5.2e-172;
 Matches 811; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 255 ACCACTTCAAGTGTGCTGCGCTCCCTCCGCAACGAGTTTGGCCAAAGAGAGCTGACAGCA 314
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QY 315 ACAAGGAGATTGAGAGCTTGGCTGCCGACCTACAGTGTCTCATTTCCCATGTTTACGA 374
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Db 70 ACAAGGAGATTGAGAGCTTGGCTGCCGACCTACAGTGTCTCATTTCCCATGTTTACGA 129
QY 375 AGATTGAGTACACCGGAGTGTGGCCATGCTGCTCAAGTACGCTGGGCCACAGCTTCTG 434
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Db 130 AGATTGAGTACACCGGAGTGTGGCCATGCTGCTCAAGTACGCTGGGCCACAGCTTCTG 189
QY 435 GGAAGAGCCCACTGTGAATCTTGAAGTACTAGTAGCCCAAGATGGAAGGTGGTAG 494
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Db 190 GGAAGAGCCCACTGTGAATCTTGAAGTACTAGTAGCCCAAGATGGAAGGTGGTAG 249
QY 495 GGGCTTGGAGCCCACTGTGTACGTGAGGAGGTGACAGTTCAGATACAGCGCTGCTGA 554
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Db	250	GGGCTTGGGACCACACTGTGTCAGTGGAGAGGTGACAGCCCAAGATACAGGCGTGTGA	309
QY	555	GGAGCTATCTCTACTGAAAGCGAGAAAGCTTATTAACCAACCGCGTCTCTCTCCACACC	614
Db	310	GGAACTCATCTCTACTGAAAGCGAGAAAGCTTATTAACCAACCGCGTCTCTCTCCACACC	369
QY	615	TCATCCGCGCCACCGTGTGGGGGCGACCAATGCAAACTCAAAATGCGTTCAAAAGGAG	674
Db	370	TCATCCGCGCCACCGTGTGGGGGCGACCAATGCAAACTCAAAATGCGTTCAAAAGGAG	429
QY	675	AGACCCACTGACTCTCCTTCTACTCTTATGCCATTGGTCCCATCTTCTTGGGGG	734
Db	430	AGACCCACTGACTCTCCTTCTACTCTTATGCCATTGGTCCCATCTTCTTGGGGG	489
QY	735	AAAAATCTAGTATTTGTATTATTGAAATCTTACAGCAACAAATAGAACTCTGAGCCA	794
Db	490	AAAAATCTAGTATTTGTATTATTGAAATCTTACAGCAACAAATAGAACTCTGAGCCA	549
QY	795	TGAGAGCTCTTGACCAAGTGAATCACCAAGCCGATACGAAGCTTGTCCCAACAAAATGTGT	854
Db	550	TGAGAGCTCTTGACCAAGTGAATCACCAAGCCGATACGAAGCTTGTCCCAACAAAATGTGT	609
QY	855	GGCAAAATGAAGTATATCAAGCAATTAATCTCCACCCCAAGGCTTGCTGTAATCTGGGACCA	914
Db	610	GGCAAAATGAAGTATATCAAGCAATTAATCTCCACCCCAAGGCTTGCTGTAATCTGGGACCA	669
QY	915	ATGATTACCTCATAGAGCGTGTGTGAGAGTTAGATGGAATACCTGTGAAAATGCGCTAGG	974
Db	670	ATGATTACCTCATAGAGCGTGTGTGAGAGTTAGATGGAATACCTGTGAAAATGCGCTAGG	729
QY	975	CAGTCCCGACCAATAGAGAGGCATTCATGAACATTTTGGCATTTAAACCAAAAATATA	1034
Db	730	CAGTCCCGACCAATAGAGAGGCATTCATGAACATTTTGGCATTTAAACCAAAAATATA	789
QY	1035	CTTGTTATCATTAATAAACTGTCATCCCAACATGAA	1068
Db	790	CTTGTTATCATTAATAAACTGTCATCCCAACATGAA	823

RESULT	7
ALJ356976/c	
LOCUS	
DEFINITION	ALJ356976 160066 bp DNA linear HTG_08-FEB-2002
ACCESSION	Homo sapiens chromosome 1 clone RP4-700P11 map p32.1-32.3, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.
VERSION	ALJ356976
KEYWORDS	ALJ356976.18 GI:18643752
SOURCE	HTG; HTGS_PHASE1; HTGS_ACTIVERPIN; HTGS_DRAFT; HTGS_FULLTOP. human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (sites)
AUTHORS	Van Hellmond,Z.
TITLE	Direct Submission
JOURNAL	Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humgen@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 10, 2002 this sequence version replaced gi:18477299.
COMMENT	

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Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
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Project Information
Center project name: dU700P11
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Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: Plasmid; 108752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 6% of reads
Dye-terminator Big Dye; 93% of reads
Consensus quality: 157881 bases at least Q40
Consensus quality: 158654 bases at least Q30
Consensus quality: 159095 bases at least Q20

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Insert size: 159666; sum-of-contigs
Insert size: 111224; 66.8% error; agarose-1p
Quality coverage: 7.58x in Q20 bases; sum-of-contigs quality
coverage: 12.72x in Q20 bases; agarose-1p
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 87143: contig of 87143 bp in length
*
* 87144 87243: gap of 100 bp
*
* 87244 94440: contig of 7197 bp in length
*
* 94441 94540: gap of 100 bp
*
* 94541 117956: contig of 23416 bp in length
*
* 117957 118056: gap of 100 bp
*
* 118057 157663: contig of 39607 bp in length
*
* 157664 157763: gap of 100 bp
*
* 157764 160066: contig of 2303 bp in length.
*
Location/Qualifiers
1..160066
source

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/clone_1fb="RPC1-4"
1..87143
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/note="assembly_fragment:01501
fragment_chain:1"
87244..94440
/misc_feature
/note="assembly_fragment:00811
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94541..117956
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118057..157663
/misc_feature
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157764..160066
/misc_feature
/note="assembly_fragment:01821"
157764..160066
BASE COUNT 42972 a 35602 c 36676 g 44415 t 401 others
ORIGIN
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	Query Match	Similarity	60.2%	Score 645.4	DB 2,	Length 160066;
	Best. Local	Similarity	99.8%	Pred. No. 7.5e-135;		
	Matches 646;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0
QY	426	AGACTTCTGGAGAGAGGCCACCTGGAACTTGTGGAACTTACCTAGTAGCCCAATGAA	485			
Db	112388	AGACTTCTGGAGAGAGGCCACCTGGAACTTGTGGAACTTACCTAGTAGCCCAATGAA	112329			
QY	486	AGGTGCTAGGGGCTTGGGACCACTGTGTCTAGTGGAGAGGTGAGACTCCAGATCCAG	545			
Db	112328	AGGTGCTAGGGGCTTGGGACCACTGTGTCTAGTGGAGAGGTGAGACTCCAGATCCAG	112269			
QY	546	CGCTCTGTGAGGAAGCTCATCTCTACTGTGAAGCGAAGACTTTAAACACCGCTCTCTCC	605			
Db	112268	CGCTCTGTGAGGAAGCTCATCTCTACTGTGAAGCGAAGACTTTAAACACCGCTCTCTCC	112209			
QY	606	TTCACACACCTCATCCCGCCACCTGTGGGGGTGACCAATGCAAACTCAATGGTCTT	665			
Db	112208	TTCACACACCTCATCCCGCCACCTGTGGGGGTGACCAATGCAAACTCAATGGTCTT	112149			
QY	666	CAAAAGGAGAGAGACCACTACTACTCTCTCTCTTACTCTTATGCCATTGTCCTCATTC	725			
Db	112148	CAAAAGGAGAGAGACCACTACTACTCTCTCTCTTACTCTTATGCCATTGTCCTCATTC	112089			
QY	726	TTCGTGGGGAGAAAAATCTAGTAATTTGATTATTTGCAATCTTACGCAACAATAGAACT	785			

Db 112088 TTGTGGGGGAAAAATCTAGTATTTTGTATTTGATTTTACAGCAAAATAGAGACT 112029
QY 786 CTTGGGCAATGAGAGCTCTTGACCACTGATGATCACAGCCGATACGAACGCTTGCCACACA 845
Db 112028 CTTGGGCAATGAGAGCTCTTGACCACTGATGATCACAGCCGATACGAACGCTTGCCACACA 111969
QY 846 AAAATGTGTGCAAAATGAGATGATATCAACCAATTAATCTCCCAAGCCGCTCTGTAA 905
Db 111968 AAAATGTGTGCAAAATGAGATGATATCAACCAATTAATCTCCCAAGCCGCTCTGTAA 111909
QY 906 CTTGGGCAATGATGATTAAGGCTGTTGTGAGATTAGATGAATACCTGTGAAA 965
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QY 966 GTGCTTGAAGAGAGTCCAGCAATAGAGGATTCATGATGATTTTTCATATTAACC 1025
Db 111848 GTGCTTGAAGAGAGTCCAGCAATAGAGGATTCATGATGATTTTTCATATTAACC 111789
QY 1026 AAAAATACTTGTATCATTAATAAACTTGATCCACATGAATTTTC 1072
Db 111788 AAAAATACTTGTATCATTAATAAACTTGATCCACATGAATTTTC 111742

RESULT 8
LOCUS BC003228 1033 bp mRNA linear ROD 12-JUL-2001
DEFINITION Mus musculus, similar to RIKEN cDNA 3110050F08 gene, clone MGC:6581
IMAGE:3483448, mRNA, complete cds.
ACCESSION BC003228
VERSION BC003228.1 GI:13096857
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus.

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL 1 (bases 1 to 1033)
Strausberg, R.
Direct Submission
Submitted (20-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalobedcm.tmc.edu,
Villalob, D.K., Luna, R.A., Hale, S.M., Huliy, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAP Plate: 6 Row: P Column: 16
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.

FEATURES
Source location/Qualifiers

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/db_xref="taxon:10090"
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/tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
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/clone_lib="NCI-CGAP_Mam5"
/lab_host="DH10B"

CDS
/note="Vector: pCMV-Sport6"
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/product="Similar to RIKEN cDNA 3110050F08 gene"
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/db_xref="GI:13096858"
/translation="MVAATVATMILLMAACAQSEDFYDFKAVNRGLVLSLEKRG
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ARTYVSFPMPSKLTAVTGTGAHAPARLYLQTSRGKPTNFMFKLYLVDPPGKYVGA
MDP
TYPVAIEIKRITREQVVKLLIRKRED"
BASE COUNT 264 a 285 c 270 g 214 t
ORIGIN
Query Match 44 1%; Score 473; DB 10; Length 1033;
Best Local Similarity 72.2%; Pred. NO. 3.1e-96;
Matches 723; Conservative 0; Mismatches 220; Indels 58; Gaps 6;
QY 2 ACGCCGCCACCTCCGGAACAAAGCCATGTCGCGCGAGCGGTGCGGCGGCTGCTC 61
Db 14 AAGTGGCCACCTCGGAGTGAACCATGTTGCAAG---CTGAGGAGAGCGGCTGCTC 70
QY 62 CTGTGGCTGCGGCTGCGCGAGAGAGAGACTTTTACACTTCAAGCGGCTAAC 121
Db 71 CTGTGGCGCGGCTGCGCGCAATCCGAGCAGACTTTCAGACTTCAAGCGGCTAAC 130
QY 122 ATCCGGGGCAAACTGCTGCTGAGAGATGACCGGAGATGCTGCTGCTGCTGAT 181
Db 131 ATCCGGGGCAAGCTGCTGCTGAGAGATGACCGGCTGCTGCTGCTGCTGCTGAT 190
QY 182 GTGGCCAGAGAGTGGGCTTACAGACAGCAGTACAGAGCGCTGACAGCTGACAG 241
Db 191 GTAGCTAGCGAATGTGCTTACAGACAGCAGTACAGAGCGCTGACAGAGCTGAC 250
QY 242 GACCTGGGCCCCCAGCACTTACAGCTGCTGCTTCCCTGCAACGAGTTGGCAAC 301
Db 251 GACCTGGGCCCCCAGCACTTACAGCTGCTGCTTCCCTGCAACGAGTTGGCAAC 310
QY 302 GAGCTGACAGCAACAGAGATGAGAGATGAGAGCTTCTGCGGACCTACAGTGTCT 361
Db 311 GAACCAAGCAACAGAGATGAGAGATGAGAGCTTCTGCGGACCTACAGTGTCT 370
QY 362 CCCATGTTAGCAAGATGAGAGATGAGAGCTTCTGCGGACCTACAGTGTCT 421
Db 371 CCCATGTTAGCAAGATGAGAGATGAGAGCTTCTGCGGACCTACAGTGTCT 430
QY 422 GCCAGACTTGTGGAAGAGAGCCAGCTGAGACTTGTGGAAGTCTTACAGTGTCT 481
Db 431 ACCAGACTTGTGGAAGAGAGCCAGCTGAGACTTGTGGAAGTCTTACAGTGTCT 490
QY 482 GGAAGGAGTGAAGGAGGCTGAGAGCCAGAGTGTGAGAGAGGAGTGTGAGATC 541
Db 491 GGAAGGAGTGAAGGAGGCTGAGAGCCAGAGTGTGAGAGAGGAGTGTGAGATC 550
QY 542 ACAGCGCTGTGAGAGAGCTATCTATCTGAGAGAGAGAGAGAGAGAGAGAGAG 601
Db 551 ACAG 599
QY 602 CTCTCCACCACTCATCCGCGCCAGCTGTGTGGGCTGAGCAATGCAAAATGCT 661
Db 600 -----CGGGTCCCTCTGAACTCCCATCCATCCGCAAACTCAAGTGT 642
QY 662 GCTTCAAG 721
Db 643 GCTTCAAG 685
QY 722 ATTCTTGGGGGAAAAATCTAGTATTTTGTATTTTGTATTTTGTATTTTGTAT 781
Db 686 -----CAGAGCAAAATCTTAGACTGTGATTTTGAATCAAGAGAGAGAGAG 738
QY 782 AACTCTGCGCAATGAGAGCTTTGACCAAGTGAATCAACAGAGAGAGAGAGAG 840
Db 739 AACTCTTGTGCGCAGTGAAGTGTCTTAACAGACATCAACAGAGAGAGAGAGAG 798

OY	841	CACAAATATGTCGGCAATAGAGTATATCAAGCATTAATCTCCACCAGGCCTCT	900
Db	799	CAGAAGAACATGTGCAAGGCTATTGAGAAACATGTAGATGTAGAGCAA-TCTCT	857
OY	901	GTAAGTGGAACATGATGTACTCATATAGGGCTGTTGTGAGGATTAGGATAAATACCTG	960
Db	858	ACCTACCGCATGCAGTAGTCTTACTCTACAGGGAGGCTGTGAGATTAGATCTAATATACCG	917
OY	961	TGAAGTGCCCT-AGGCATGTGCCAGCCAATAGAGGCATTC	1000
Db	918	TGAACACGCTGTGGGCGCAGTCTAGTCGAAGGGAGACACTC	958
RESULT	9		
AF322456			
LOCUS	AF322456	51381 bp DNA linear HTG 06-DEC-2000	
DEFINITION	Homo sapiens chromosome 17 clone BAC629910 map 17p13.3, ***		
ACCESSION	AF322456		
VERSION	AF322456.1 GI:11559861		
KEYWORDS	HTG; PHASEL.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 51381)		
	Zhao,X.T., He,M., Wan,D.F., Ye,Y., Qin,W.X., Huang,Y., Zuo,L. and Gu,J.R.		
TITLE	Gene clone on human chromosome 17p13.3		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 51381)		
AUTHORS	Zhao,X.T., He,M., Wan,D.F., Ye,Y., Qin,W.X., Huang,Y., Zuo,L. and Gu,J.R.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-NOV-2000) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie-tu Road, Shanghai 200032, P. R. China		
COMMENT	* NOTE: This is a 'working draft' sequence. It currently consists of 120 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.		
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*		gap of unknown length	
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*		gap of unknown length	
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*	27588	27796:	contig of 209 bp in length
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*	32404	33056:	contig of 653 bp in length
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40.6%: Score 435.4; DB 2; length 51381;			
88.1%: Pred. No. 1.4e-87;			
Best Local Similarity			

	Matches	483:	Conservative	0:	Mismatches	64:	Indels	1:	Gaps	17:
QY	136	GGTGTGCGTGGAGAAAGTACCGCGGATTCGGTGTGCCGTGTGTGTGAATGTGGCAGCGAGTG	195							
Db	50834	GGTGTGCGTGGAGAAAGTACCGCGGATTCGGTGTGCCGTGTGTGAATGTGGCAGCGAGTG	50893							
QY	196	CGGGCTTTCACAGACCAGCACTACCGAGGCCCTGAGCAGCTGGCAGCGAGACCTGGGCCCA	255							
Db	50894	CGGGCTTTCACAGACCAGCACTACCGAGGCCCTGAGCAGCTGGCAGCGAGACCTGGGCCCA	50953							
QY	256	CCACTTTCAACTGCTGCCTTCCTCCCTGCACACAGTTTGGCCAAACAGAGACTGACAGCA	315							
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QY	316	CAGAGAGATTGAGAGCTTTGGCTGCCGCACTACAGTGTCTCATTTCCCATSTTTAGCAA	375							
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QY	376	GATTTCAGTCAACCGGTACTAGTGGTCCCATTCCTGCTTCAAGTACCTGCGCCACACTTCTGG	435							
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QY	496	GGCTTTGGAGCCCACTGTGTCTAGTGGAGGAGGTCAAGTCTCAAGATCACAGCGCTCGTGA	555							
Db	51194	GGCTTTGGAGCCCACTGTGTGTCTAGTGGAGGAGGTCAAGATCACAGCGCTCGTGA	51253							
QY	556	GAAAGTCATACCTACAGAACGAGAGAGACTTAATACCAACGCGCTCCTCTCCACACACT	615							
Db	51254	GAAAGTCATACCTACAGAACGAGAGAGACTTAATACCAACGCGCTCCTCTCCACACACT	51312							
QY	616	CATCCCGCCCACTGTGTGGGGCTGACCAATGCACAACTCAAAATGTGTCTTCAAGAGGACA	675							
Db	51313	CATCCCGCCCACTGTGTGGGGCTGACCAATGCACAACTCAAAATGTGTGTCTTCAAGAGGACA	51372							
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Db	51373	GACCCACT 51380								

RESULT	10				
AX186595/C					
LOCUS	AX186595	751 bp	DNA		
DEFINITION	Sequence	2290 from Patent WO0142467.			
ACCESSION	AX186595				
VERSION	AX186595.1	GI:15138034			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 751)				
JOURNAL	Schlegel, R., Deeds, J., Berger, A. and Zhao, X.				
	Genes, compositions, kits, and methods for identification,				
	assessment, prevention, and therapy of cervical cancer				
	Patent: WO 0142467-A 2290 14-JUN-2001;				
	Millennium Predictive Medicine, Inc. (US)				
FEATURES	Location/Qualifiers				
Source	1..751				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
BASE COUNT	194 a	141 c	143 g	269 t	4 others
ORIGIN					

Query Match	37.9%	Score 406.2,	DB 6;	Length 751;
Best Local Similarity	99.1%	Pred. No. 3.4e-81;		
Matches 419;	Conservative	0;	Mismatches 3;	Indels 1;
				Gaps 1.

Db	745	AACTCAATGGGTGGCTTC-AAGGAGAGACCCACTGACTCTCCCTTCCTTACTCTTATGCC	687
QY	710	ATTGGTCCCATCATTTCTGTGGGGAAAAAATTCAGTATTTTGATTTATTTGAAATCTTACA	769
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QY	770	GCACCAAAATAGGAACCTCCTGGCCCAATGAGAGCTCTTGACCAAGTGAATCAGCAGCCGATAC	829
Db	626	GCACCAAAATAGGAACCTCCTGGCCCAATGAGAGCTCTTGACCAAGTGAATCAGCAGCCGATAC	567
QY	830	GAAGCTCTTGCCACACAAAATGTGTGGCAAAATAGAAATATCAAGCAATATCTCCAC	889
Db	566	GAAGCTCTTGCCACACAAAATGTGTGGCAAAATAGAAATATCAAGCAATATCTCCAC	507
QY	890	CCAAAGCTTCGTAAACGTGGGACCAATATTAACCATAGAGGCTGTGTGAGGATTTAGA	949
Db	506	CCAAAGCTTCGTAAACGTGGGACCAATATTAACCATAGAGGCTGTGTGAGGATTTAGA	447
QY	950	TGAATTAACCTGTGAAGAAGTCCAGAGCACTGCCAGCCAAATAGSAGAGCTTCAATGAACAT	1009
Db	446	TGAATTAACCTGTGAAGAAGTCCAGAGCACTGCCAGCCAAATAGSAGAGCTTCAATGAACAT	387
QY	1010	TTTTTGCATATTAACCAAAAAAATAAATTGTATCAATTAATAAAACCTTGCAATCAACATGAAT	1069
Db	386	TTTTTGCATATTAACCAAAAAAATAAATTGTATCAATTAATAAAACCTTGCAATCAACATGAAT	327
QY	1070	TTC 1072	
Db	326	TTC 324	

RESULT	11				
LOCUS	AX187668/c				
DEFINITION	AX187668	468 bp	DNA		linear
ACCESSION	Sequence 3363 from Patent WO0142467.				PAT 06-AUG-2001
VERSION	AX187668				
KEYWORDS	AX187668.1	GI:15139132			
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 468)				
AUTHORS	Schlegel, R., Deeds, J., Berger, A. and Zhao, X.				
TITLE	Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy for cervical cancer				
JOURNAL	Patent: WO 0142467-A 3363 14-JUN-2001;				
	Millennium Predictive Medicine, Inc. (us)				
FEATURES	Location/Qualifiers				
source	1..468				
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BASE COUNT	131 a	84 c	94 g	159 t	
ORIGIN					

Query Match	33.2%;	Score 356;	DB 6;	Length 468;
Best Local Similarity	100.0%;	Pred. No. 6.6e-70;		
Matches 356;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	717	CCATCATCTCTGTGGGGGAAAAAATTCAGATATTTTGAATTTATTTGAATCTTACAGCAACA	776
Db	468	CCATCATCTCTGTGGGGGAAAAAATTCAGATATTTTGAATTTATTTGAATCTTACAGCAACA	409
QY	777	ATAGAACTCTGGGCCATGAGACTCTTGACCGTAAATCACCAGCCATACGAACGTC	836
Db	408	ATAGAACTCTGGGCCATGAGACTCTTGACCGTAAATCACCAGCCGATACGAACGTC	349
QY	837	TTGCCAAGAAAAATGTGTGGCAATTAAGAATATCAAGCAATATATCTCCACCACCAAGC	896
Db	348	TTGCCAAGAAAAATGTGTGGCAATTAAGAATATCAAGCAATATATCTCCACCACCAAGC	289

[illegible][illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
1 (bases 1 to 51381)	Zhao, X.T., He, M., Wan, D.F., Ye, Y., Qin, W.X., Huang, Y., Zuo, L. and Gu, J. R.	Gene clone on human chromosome 17p13.3	Unpublished	
2 (bases 1 to 51381)				

TITLE	Direct Submission
JOURNAL	Submitted (21-NOV-2000) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie-Tu Road, Shanghai 200032, P. R. China
COMMENT	* NOTE: This is a 'working draft' sequence. It currently

COMMENT

* NOTE: This is a 'working draft' sequence. It currently
* consists of 120 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

*	1	236:	contig of 236 bp in length
*			gap of unknown length
*	237	435:	contig of 199 bp in length
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*	436	665:	contig of 230 bp in length
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*	666	879:	contig of 214 bp in length
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*	880	1121:	contig of 242 bp in length
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*	1122	1948:	contig of 827 bp in length
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*	3230	3893:	contig of 664 bp in length
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*	4273	4420:	contig of 148 bp in length
*			gap of unknown length
*	4421	4633:	contig of 213 bp in length
*			gap of unknown length
*	4634	5219:	contig of 586 bp in length
*			gap of unknown length

* 5220 5881: contig of 662 bp in length
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* 5882 6118: contig of 237 bp in length
* gap of unknown length
* 6119 6334: contig of 216 bp in length
* gap of unknown length
* 6335 6484: contig of 150 bp in length
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* 6485 6623: contig of 139 bp in length
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* 6624 6861: contig of 238 bp in length
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* 6862 7067: contig of 206 bp in length
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* 7068 7836: contig of 769 bp in length
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* 7837 8541: contig of 705 bp in length
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* 8542 8731: contig of 190 bp in length
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* 8732 8875: contig of 144 bp in length
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* 8876 9094: contig of 219 bp in length
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* 9685 10350: contig of 666 bp in length
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* 18324 18532: contig of 209 bp in length
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* 31588 31792: gap of unknown length
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* contig of 653 bp in length
* 33057 33266: gap of unknown length
* contig of 210 bp in length
* 33267 33471: gap of unknown length
* contig of 205 bp in length
* 33472 34137: gap of unknown length
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* 34138 34789: gap of unknown length
* contig of 652 bp in length
* 34790 35003: gap of unknown length
* contig of 214 bp in length

Query Match 24.4%; Score 261.8; DB 2; Length 51381;
Best Local Similarity 80.3%; Pred. No. 1.9e-48;
Matches 380; Conservative 0; Mismatches 87; Indels 6; Gaps 6;

OY 403 TCCTGCTTCAAGTACCTGGCCAGACTTTCG 435
 DB 134838 CCTGCTTCAAGTACCTGAGCTTG 134806
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 LOCUS
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 IMAGE:3988837, mRNA, complete cds.
 ACCESSION BC019664
 VERSION BC019664.1 GI:18044309
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1047 bp mRNA linear ROD 22-JAN-2002
 1 (bases 1 to 1047)
 Strausberg, R.
 Direct Submission
 Submitted (19-DEC-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgc.ncl.nih.gov
 Contact: MGC help desk
 Email: cgaabbs@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: http://www.hgsc.bcm.tmc.edu/cdna/
 Contact: amgebcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Huiy, S.W., Hale, S.M.,
 Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
 Richards, S., Gibbs, R.A.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
 Series: IRAC Plate: 40 Row: 1 Column: 9
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis.
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 Location/Qualifiers
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 /db_xref="taxon:10090"
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 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"
 13. 642
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 /db_xref="GI:18044310"
 /translation="MEPEAPYPLKCSGPKAKIFAVILSMVLCTVAFLLQELFKPRT
 NSPYSEYKDAKGRVSLSEKFKASLVANASDQRFDKSYQILREHKREGPYHN
 VIAPPCNGFSGSPKSKSEKESFARONGVTFPIFKIKILGPEKPEPRFRTVDSKK
 EPRNFNTKYLVPESQGVKFWPEPELEAIRPHVSOIMGQILLKKEDL"
 BASE COUNT
 ORIGIN
 342 a 221 c 227 g 257 t
 16 5%: Score 177.2; DB 10; Length 1047;
 Best Local Similarity 59.6%; Pred.No.1.4e-29;
 Matches 299; Conservative 0; Mismatches 203; Indels 0; Gaps 0;

OY 97 CTTTACGACTTCAAGGGGTCACATCCGGGCAAACTGCTGTGCGAGAACTACCG 156
 DB 150 CTTTACTCTCTTGAAGTAAGATGCCAAGAAAGAACCGCTGTCTGTGAAAAGTTCA 209
 OY 157 CGGATCGGTGTCCTGTGTGTGATGTGGCCAGGAGTGGGCTTCACAGCCAGCACTA 216
 DB 210 AGGCAAGGCTTCCCTGGTGTGAACGCTGTGAGTACTGCCCTCAGCAGCAAGATGA 269
 OY 217 CCGAGCCCTGCAAGAGCTGACGAGTGGGCCCCCAGCACTTCACAGTCTGGCCTT 276
 DB 270 CCAGATTCTCAAGGAGCTACACAGAGAGTTCGGGCCCTATCACTTCAAGCTGCTG 329
 OY 277 CCCCTGACAGCAGTTGGGCAACAGAGCCTGACACAGAGATGAGAGCTTTCG 336
 DB 330 CCCGTGCAATCAGTTTGGAGAAATCGAGGCCAAGTCCAGCAAGAGAGTGAATCTTTTC 389
 OY 337 CTGCGGCACTACAGTGTCTCATTTCCCAATGTTAGCAAGATTCAGTCCGTAAGT 396
 DB 390 GAGACAGAACTACGAGATCAGATTCCTCCATCCAGATTAAGATTAGAGCGCGGA 449
 OY 397 TGGCCATCTGCTTCAAGTACCTGCGCCAGACTTCTGGGAAGAGCCACCTGAGACTT 456
 DB 450 AGCAGAACTGCGGTTAGATTATGTTGATCTTCCAAAGAGGAGCCAAAGGTGAAATT 509
 OY 457 CTGGAAGTACTAGTAGCCCAAGATGAAAGTGTGAGGGCTGTGGAGCCAACTGTGTC 516
 DB 510 TTGGAAAGTATCTGCTGCAACCTGAGGAGACAGTCTGGAAGTCTGAGGCCAGAAAGACC 569
 OY 517 AGTGAAGAGGTGACAGCTCAGATCAGACAGCGCTGTGAGAAAGCTCATCTGTAAGCG 576
 DB 570 CCTTGAAGCCATCAGACGCTCATGTATCACAATGATTGGCAAAATTATCTTAAAAAGAA 629
 OY 577 AGAAGACTATATACCAACCGCT 598
 DB 630 AGAGGATCTATGAACCAACCGT 651
 RESULT 15
 AC022847/c
 LOCUS
 DEFINITION Homo sapiens chromosome 11 clone RP11-261F7 map 11, LOW-PASS
 SEQUENCE SAMPLING.
 ACCESSION AC022847
 VERSION AC022847.1 GI:6922212
 KEYWORDS
 SOURCE HTGS_PHASE0.
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 55891)
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 Homo sapiens chromosome 11, clone RP11-261F7
 Unpublished
 2 (bases 1 to 55891)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Beckler, R., Bedalov, F.,
 Boguslavsky, L., Bouhgalter, B., Brown, A., Burkett, G., Castle, A.,
 Choepe, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
 DeArrelano, K., Dewar, K., Domino, M., Doyle, M., Fensholt, J.,
 Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
 Gardina, S., Grant, G., Hages, B., Heaford, A., Horton, L.,
 Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
 Landers, T., Lechoczky, J., Levine, R., Liu, C., Liu, G., Locke, K.,
 Macdonald, P., Marquis, N., McEwan, P., McKernan, A., McKernan, K.,
 McPherson, R., Meldrum, J., Meneus, L., Morrow, J., Naylor, J.,
 Norman, C.H., O'Connor, T., O'Donnell, P., Ollivier, T.M., Peterson, R.,
 Plierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rotman, D.,
 Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
 Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
 Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W., J.,
 Zimmer, A. and Zody, M.
 Direct Submission

JOURNAL
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR

Web site: <http://www-seq.wi.mit.edu>

----- Project Information
Contact: sequence_submissions@genome.wi.mit.edu

Center project name: 16164

Center clone name: 261_F_7

* NOTE: This record contains 78 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 698: contig of 698 bp in length
* gap of unknown length
* 699 1436: contig of 738 bp in length
* gap of unknown length
* 1437 2155: contig of 719 bp in length
* gap of unknown length
* 2156 2866: contig of 711 bp in length
* gap of unknown length
* 2867 3559: contig of 693 bp in length
* gap of unknown length
* 3560 4266: contig of 707 bp in length
* gap of unknown length
* 4267 4955: contig of 689 bp in length
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* 4956 5656: contig of 701 bp in length
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* 5657 6372: contig of 716 bp in length
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* 6373 7082: contig of 710 bp in length
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* 16428 17145: contig of 718 bp in length
* gap of unknown length

* 17146 17851: contig of 706 bp in length
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* 18566 19394: contig of 829 bp in length
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* 22285 23015: contig of 731 bp in length
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* 23016 23739: contig of 724 bp in length
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* 23740 24445: contig of 706 bp in length
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* 24446 25157: contig of 712 bp in length
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* 40910 41609: contig of 700 bp in length
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*      *      *      *      *      *      *      *      *
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*      *      *      *      *      *      *      *      *
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Query Match 16.3%; Score 174.6; DB 2; Length 55891;
 Best Local Similarity 95.2%; Pred. No. 8.4e-29;
 Matches 180; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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DB 33732 GGGCCCCCACCCTTCAACGTGCTGCGCTTCCCTGCACACAGTTTGGCCACAGAGAGCCT 33673
QY 308 GACAGCAACAGAGAGATTGAGAGCTTTGCGCTGCGGACCTACAGTGTCTCATTTCCCATG 367
DB 33672 GACAGCAACAGAGAGATTGAGAGCTTTGCGGCGGACCTACAGTGTCTCATTTCCCATG 33613
QY 368 TTTAGCAAGATTGACGTACCGGTACTGGTCCCATCCCTTCAGTACAGTACCTGGCCAG 427
DB 33612 TTTAGCAAGATTGACGTACCGGTACTGGTCCCATCCCTTCAGTACAGTACCTGGCCAG 33553
QY 428 ACTTCTGGG 436
DB 33552 AAGTCTGG 33544

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Search completed: August 25, 2002, 06:13:42
 Job time: 6922 sec

